



APPLIED MATHEMATICS COLLOQUIUM: Discovering the dynamics of RNA splicing from spatial snapshots

Chris Miles

Assistant Professor of Mathematics
UC Irvine

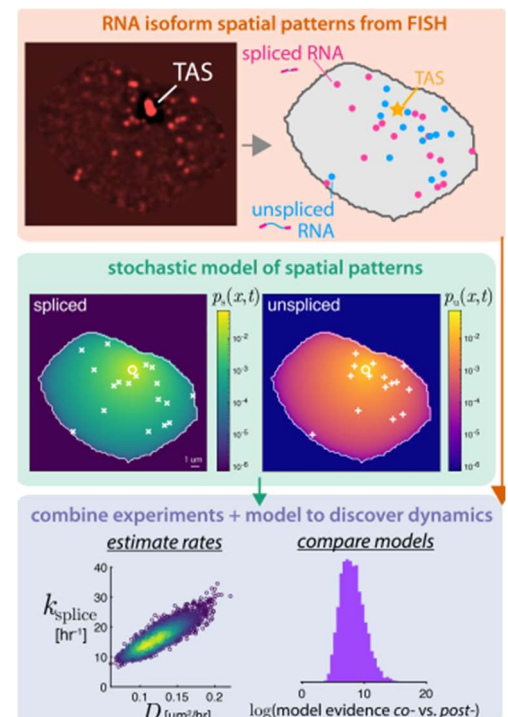


About The Speaker:

Dr. Christopher Miles is an Assistant Professor of Mathematics at UC Irvine, where he is also affiliated with the Center for Complex Biological Systems and the NSF-Simons Center for Multiscale Cell Fate. He was the Morawetz Fellow and a Courant Instructor at the Courant Institute at NYU and received his Ph.D. from the University of Utah. Before all of that, he grew up in Pennsylvania and is a first-generation scholar, with no family member having attended college. In rare instances of free time, he likes to climb rocks, eat vegan food, and care for foster kittens.

Abstract:

Splicing is a foundational component of gene expression. This molecular process modifies the information encoded in pre-mRNA after they are transcribed from DNA blueprints, resulting in the translation of proteins with completely different functions arising from the same gene. Despite enormous progress in understanding splicing, the inability to directly image the process has prevented the understanding of several key aspects, including a 40-year-long debate about the timing of splicing relative to transcription. In collaboration with the Fangyuan Ding lab of Biomedical Engineering at UCI, I will discuss our work combining imaging, math modeling, and statistical inference to understand splicing from imaging data alone. The key idea is to write down a mechanistic spatial stochastic model (Spatial Cox process) for the individual RNA positions. The positions are obtained from experimental images, and the dynamic rates are inferred from static snapshots using Variational Bayesian inference. I'll also talk about Bayesian model selection and optimal experimental design.



Date:
10/14/2022

Time:
3:00 PM - 5:20 PM

Location:
SSB 170

For more information, contact : Lihong Zhao
lzhao33@ucmerced.edu